



PCT10

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/019,098

DATE: 01/22/2002

TIME: 13:19:06

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Output Set: N:\CRF3\01182002\J019098.raw

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4 <110> APPLICANT: HAFEN, Ernst
6 <120> TITLE OF INVENTION: In vivo model system for type-2 diabetes
8 <130> FILE REFERENCE: 27656/38053
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/019,098
C--> 11 <141> CURRENT FILING DATE: 2001-12-20
13 <150> PRIOR APPLICATION NUMBER: PCT/IB99/01166
14 <151> PRIOR FILING DATE: 1999-06-22
16 <160> NUMBER OF SEQ ID NOS: 4
18 <170> SOFTWARE: PatentIn Ver. 2.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 2907
22 <212> TYPE: DNA
23 <213> ORGANISM: Drosophila melanogaster
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30 tactacgata ccgaaaagaa gttcctgcaa agagccgagc caaaaagggt tatatatctg 180
32 aagaattgct tcaacatcaa tcgcggtttg gacaccaagc atagatttgt cattgtgctc 240
34 tctccagag acggtggatt cggcatcggt ctgagaaacg aaaatgattt acgcaaattg 300
36 ttggacaaac tactagtctt acaaaggaac atagccaatt cgaatggaac agcgcaactca 360
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40 atcacgggaa cctaccactg ttgccttact tcaaaatccc tgacattcgt gtgcattgga 480
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48 atgcacaaca cgatactgag cgctatgtca gccaaaacag agtcgaacac gaatttaata 720
50 aacgtttatc agaatagacc tgacttaagt cagagcccca tgagaaagcg atcgtcgtct 780
52 gcaaacgaag catcgaagcc gataaacgta aatgtcatac aaaatagtca aaactctctc 840
54 gaattgcgca gctgcagttc gccccataac tatggtttcg gcagagagag atgcgatagc 900
56 ttaccaacca gaaatggaac cctaagcgag tccagcaatc aaacgtactt tggttccaac 960
58 catggactgc gatccaatac tatactctggc atcgtctcgc actcaacca caagcatagt 1020
60 aatagtccaa cgttcaccat gccattaaga tgcacgaat ccgaagagtc atcaattagt 1080
62 gtcgatgaat ccgacgacaa cggcagtttt agccactaca gattaaacac gcggtcatct 1140
64 gagacggcaa ttcctgagga aaacattgat gactttgcca gtgcggaatt atttagcaaa 1200
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84 gcaaccaatt tggaaaagca gaagttcatc aagaataatg aaattccgaa atacattgaa 1800
86 aacgtgttcc caaaagcccc gcgaacggat agtccagcc taactctgca cgccacaagt 1860
88 caaaaggaca ttttcaatgg caccaaacta aataacactg cgatcacatc cgaggatggg 1920
90 tacctcgaga tgaagccagt cggtaatgga tacactccca gttcgaattg cctgccaatg 1980
92 aaagtggaga aactcaagct atccgactat cagacagcac cgccactcac cgcaacagcc 2040
94 gcaccagtgc acgattttaa caaaattagc acatacaata tatccgctga gaaatggaga 2100
96 gaacagccca gcagaagcga ggaaaagaag tcgaactcgc cattgaatga caacaccttt 2160
98 agctcgaaac ccacaaatgt cgagagtaca agcaaaagcc atgatgttca ttcagcaaatt 2220
100 caaattgatt gcgagaaaagt gtgcgcgcag agcagcgata agctaaataa tcatctggcc 2280
102 gacaagattg tcgagaacaa caatttggat ataggcgggc atgaggaaaa gaagttgggt 2340
104 cattcgataa gcagcgaaga ctacacacaa atcaaggaca aatcgaatga tttcacaaaa 2400
106 tttaacgaag cgggtacaaa aattctgcaa attaaaagcg acagctcact catctcatcg 2460
108 aagctatacc aaaaggggat acacaaggat aacttgagag gttcgcagag acttacagag 2520
110 agtgtgaata cgattcccga taatgccacc gccaccgcgg tgagcagcag ctactcacc 2580
112 aaattcaata taaattcagc aaagccagcc gccgcgcggc attcgcgtag cactggcaca 2640
114 gatccaagta caccacagaa cattctacag attaaagatt tgaatttccc ctcaaggtcg 2700
116 tcgtctcgca tatcccagcc ggagctgcac tacgccagcc tagatcttcc ccattgcagt 2760
118 ggccaaaatc cagctaaata cctgaagaga ggatcacgcg aatcgccgcc ggtgtccgca 2820
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141 1 5 10 15
143 aag ctg aag acc atg aag aag aag ttc ttt gtg ctg tac gag gag acg 96
144 Lys Leu Lys Thr Met Lys Lys Lys Phe Phe Val Leu Tyr Glu Glu Thr
145 20 25 30
147 agc act tcg gca gcc cgg ctg gag tac tac gat acc gaa aag aag ttc 144
148 Ser Thr Ser Ala Ala Arg Leu Glu Tyr Tyr Asp Thr Glu Lys Lys Phe
149 35 40 45
151 ctg caa aga gcc gag cca aaa agg gtt ata tat ctg aag aat tgc ttc 192
152 Leu Gln Arg Ala Glu Pro Lys Arg Val Ile Tyr Leu Lys Asn Cys Phe
153 50 55 60
155 aac atc aat cgc cgt ttg gac acc aag cat aga ttt gtc att gtg ctg 240
156 Asn Ile Asn Arg Arg Leu Asp Thr Lys His Arg Phe Val Ile Val Leu
157 65 70 75 80
159 tcc tcc aga gac ggt gga ttc ggc atc gtt ctg gag aac gaa aat gat 288
160 Ser Ser Arg Asp Gly Gly Phe Gly Ile Val Leu Glu Asn Glu Asn Asp
161 85 90 95
163 tta cgc aaa tgg ttg gac aaa cta cta gtt cta caa agg aac ata gcc 336
164 Leu Arg Lys Trp Leu Asp Lys Leu Leu Val Leu Gln Arg Asn Ile Ala
165 100 105 110

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168	Asn	Ser	Asn	Gly	Thr	Ala	His	Ser	Pro	Tyr	Asp	His	Val	Trp	Gln	Val	
169			115					120					125				
171	gtc	att	caa	aag	aag	ggt	att	tcg	gag	aaa	gtt	gga	atc	acc	gga	acc	432
172	Val	Ile	Gln	Lys	Lys	Gly	Ile	Ser	Glu	Lys	Val	Gly	Ile	Thr	Gly	Thr	
173		130					135					140					
175	tac	cac	tgt	tgc	ctt	act	tca	aaa	tcc	ctg	aca	ttc	gtg	tgc	att	gga	480
176	Tyr	His	Cys	Cys	Leu	Thr	Ser	Lys	Ser	Leu	Thr	Phe	Val	Cys	Ile	Gly	
177	145					150				155						160	
179	ccg	gag	aag	acg	ccc	aat	ggc	gag	gat	cgc	gtt	gcg	agc	att	gaa	ata	528
180	Pro	Glu	Lys	Thr	Pro	Asn	Gly	Glu	Asp	Arg	Val	Ala	Ser	Ile	Glu	Ile	
181					165				170						175		
183	ctt	ttg	acc	acg	atc	agg	cga	tgc	ggt	cat	gca	tcc	cca	caa	tgt	ata	576
184	Leu	Leu	Thr	Thr	Ile	Arg	Arg	Cys	Gly	His	Ala	Ser	Pro	Gln	Cys	Ile	
185			180						185					190			
187	ttc	tac	gtg	gaa	ctt	ggc	cgc	caa	agt	gtc	ttg	gga	tct	ggt	gat	ctg	624
188	Phe	Tyr	Val	Glu	Leu	Gly	Arg	Gln	Ser	Val	Leu	Gly	Ser	Gly	Asp	Leu	
189			195					200					205				
192	tgg	atg	gag	acg	gat	aac	gca	gct	att	gct	act	aat	atg	cac	aac	acg	672
193	Trp	Met	Glu	Thr	Asp	Asn	Ala	Ala	Ile	Ala	Thr	Asn	Met	His	Asn	Thr	
194		210					215					220					
196	ata	ctg	agc	gct	atg	tca	gcc	aaa	aca	gag	tcg	aac	acg	aat	tta	ata	720
197	Ile	Leu	Ser	Ala	Met	Ser	Ala	Lys	Thr	Glu	Ser	Asn	Thr	Asn	Leu	Ile	
198	225					230					235					240	
200	aac	gtt	tat	cag	aat	aga	cct	gac	tta	agt	cac	gag	ccc	atg	aga	aag	768
201	Asn	Val	Tyr	Gln	Asn	Arg	Pro	Asp	Leu	Ser	His	Glu	Pro	Met	Arg	Lys	
202				245					250						255		
204	cga	tcg	tcg	tct	gca	aac	gaa	gca	tcg	aag	ccg	ata	aac	gta	aat	gtc	816
205	Arg	Ser	Ser	Ser	Ala	Asn	Glu	Ala	Ser	Lys	Pro	Ile	Asn	Val	Asn	Val	
206				260					265					270			
208	ata	caa	aat	agt	caa	aac	tct	ctc	gaa	ttg	cgc	agc	tgc	agt	tcg	ccc	864
209	Ile	Gln	Asn	Ser	Gln	Asn	Ser	Leu	Glu	Leu	Arg	Ser	Cys	Ser	Ser	Pro	
210			275					280					285				
212	cat	aac	tat	ggt	ttc	ggc	aga	gag	aga	tgc	gat	agc	tta	cca	acc	aga	912
213	His	Asn	Tyr	Gly	Phe	Gly	Arg	Glu	Arg	Cys	Asp	Ser	Leu	Pro	Thr	Arg	
214		290					295					300					
216	aat	gga	acc	cta	agc	gag	tcc	agc	aat	caa	acg	tac	ttt	ggt	tcc	aac	960
217	Asn	Gly	Thr	Leu	Ser	Glu	Ser	Ser	Asn	Gln	Thr	Tyr	Phe	Gly	Ser	Asn	
218	305					310					315					320	
220	cat	gga	ctg	cga	tcc	aat	act	ata	tct	ggc	atc	cgt	ccg	cac	tca	acc	1008
221	His	Gly	Leu	Arg	Ser	Asn	Thr	Ile	Ser	Gly	Ile	Arg	Pro	His	Ser	Thr	
222				325						330					335		
224	aac	aag	cat	agt	aat	agt	cca	acg	ttc	acc	atg	cca	tta	aga	tgc	tca	1056
225	Asn	Lys	His	Ser	Asn	Ser	Pro	Thr	Phe	Thr	Met	Pro	Leu	Arg	Cys	Ser	
226				340					345					350			
228	gaa	tcc	gaa	gag	tca	tca	att	agt	gtc	gat	gaa	tcc	gac	gac	aac	ggc	1104
229	Glu	Ser	Glu	Glu	Ser	Ser	Ile	Ser	Val	Asp	Glu	Ser	Asp	Asp	Asn	Gly	
230			355					360					365				
232	agt	ttt	agc	cac	tac	aga	tta	aac	acg	cgg	tca	tct	gag	acg	gca	att	1152

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236	cct	gag	gaa	aac	att	gat	gac	ttt	gcc	agt	gcg	gaa	tta	ttt	agc	aaa	1200
237	Pro	Glu	Glu	Asn	Ile	Asp	Asp	Phe	Ala	Ser	Ala	Glu	Leu	Phe	Ser	Lys	
238	385					390						395				400	
240	gtc	acc	gaa	caa	aat	gta	agt	gac	gaa	aac	tac	ata	ccg	atg	aat	cca	1248
241	Val	Thr	Glu	Gln	Asn	Val	Ser	Asp	Glu	Asn	Tyr	Ile	Pro	Met	Asn	Pro	
242					405					410					415		
244	gtc	aat	cct	acc	gat	gct	atc	cat	gaa	aag	gag	aag	gct	gat	atg	cag	1296
245	Val	Asn	Pro	Thr	Asp	Ala	Ile	His	Glu	Lys	Glu	Lys	Ala	Asp	Met	Gln	
246				420						425					430		
248	aga	ttg	gaa	gat	gct	tcg	ctg	cat	ttc	aac	ttt	ccg	gag	cac	gcg	tcg	1344
249	Arg	Leu	Glu	Asp	Ala	Ser	Leu	His	Phe	Asn	Phe	Pro	Glu	His	Ala	Ser	
250			435						440						445		
252	gaa	aag	ctt	gct	aag	gat	ttt	gat	ctg	gac	tct	gat	aac	caa	tgc	tgt	1392
253	Glu	Lys	Leu	Ala	Lys	Asp	Phe	Asp	Leu	Asp	Ser	Asp	Asn	Gln	Cys	Cys	
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256	cgt	ccc	att	cgc	gcc	tat	tcg	ata	ggc	aac	aag	gtt	gag	cat	tta	aag	1440
257	Arg	Pro	Ile	Arg	Ala	Tyr	Ser	Ile	Gly	Asn	Lys	Val	Glu	His	Leu	Lys	
258	465					470					475					480	
260	ttt	aat	aag	cgc	ctg	gga	cac	ttg	aat	gat	acg	gga	cag	aat	ccg	aat	1488
261	Phe	Asn	Lys	Arg	Leu	Gly	His	Leu	Asn	Asp	Thr	Gly	Gln	Asn	Pro	Asn	
262				485							490					495	
264	cgc	gtg	cga	gcc	tac	tcg	gtt	ggc	tcc	aaa	tcg	aag	ata	ccg	cgc	tgc	1536
265	Arg	Val	Arg	Ala	Tyr	Ser	Val	Gly	Ser	Lys	Ser	Lys	Ile	Pro	Arg	Cys	
266				500						505					510		
268	gac	ctg	cag	cga	gtg	gtc	ctc	gtg	gag	gac	aat	aaa	cat	gag	ttc	aca	1584
269	Asp	Leu	Gln	Arg	Val	Val	Leu	Val	Glu	Asp	Asn	Lys	His	Glu	Phe	Thr	
270			515					520					525				
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273	Ala	Asn	Arg	Ser	Gln	Ser	Ser	Ile	Thr	Lys	Glu	Gly	Thr	Ser	Tyr	Gly	
274		530						535					540				
276	agc	agt	gcc	aat	cga	caa	aag	aag	tcc	aca	agt	gct	cca	ctc	ctc	agt	1680
277	Ser	Ser	Ala	Asn	Arg	Gln	Lys	Lys	Ser	Thr	Ser	Ala	Pro	Leu	Leu	Ser	
278	545					550					555					560	
280	ctg	aag	aac	cag	ata	aac	tcc	gac	cga	atg	agt	gac	tta	atg	gaa	att	1728
281	Leu	Lys	Asn	Gln	Ile	Asn	Ser	Asp	Arg	Met	Ser	Asp	Leu	Met	Glu	Ile	
282					565						570					575	
284	gat	ttt	tca	caa	gca	acc	aat	ttg	gaa	aag	cag	aag	ttc	atc	aag	aat	1776
285	Asp	Phe	Ser	Gln	Ala	Thr	Asn	Leu	Glu	Lys	Gln	Lys	Phe	Ile	Lys	Asn	
286				580						585					590		
288	aat	gaa	att	ccg	aaa	tac	att	gaa	aac	gtg	ttc	cca	aaa	gcc	ccg	cga	1824
289	Asn	Glu	Ile	Pro	Lys	Tyr	Ile	Glu	Asn	Val	Phe	Pro	Lys	Ala	Pro	Arg	
290			595						600					605			
292	acg	gat	agc	tcc	agc	cta	act	ctg	cac	gcc	aca	agt	caa	aag	gac	att	1872
293	Thr	Asp	Ser	Ser	Ser	Leu	Thr	Leu	His	Ala	Thr	Ser	Gln	Lys	Asp	Ile	
294		610						615					620				
296	ttc	aat	ggc	acc	aaa	cta	aat	aac	act	gcg	atc	aca	tcc	gag	gat	ggt	1920
297	Phe	Asn	Gly	Thr	Lys	Leu	Asn	Asn	Thr	Ala	Ile	Thr	Ser	Glu	Asp	Gly	

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302			645		650		655	
304	tgc ctg cca atg aaa gtg gag aaa ctc aag cta tcc gac tat cag aca	2016						
305	Cys Leu Pro Met Lys Val Glu Lys Leu Ser Asp Tyr Gln Thr							
306			660		665		670	
308	gca ccg cca ctc acc gca aca gcc gca cca gtg cac gat tta aac aaa	2064						
309	Ala Pro Pro Leu Thr Ala Thr Ala Ala Pro Val His Asp Leu Asn Lys							
310			675		680		685	
312	att agc aca tac aat ata tcc gct gag aaa tgg aga gaa cag ccc agc	2112						
313	Ile Ser Thr Tyr Asn Ile Ser Ala Glu Lys Trp Arg Glu Gln Pro Ser							
314			690		695		700	
316	aga agc gag gaa aag aag tcg aac tcg cca ttg aat gac aac acc ttt	2160						
317	Arg Ser Glu Glu Lys Lys Ser Asn Ser Pro Leu Asn Asp Asn Thr Phe							
318	705		710		715		720	
320	agc tcg aaa ccc aca aat gtc gag agt aca agc aaa agc cat gat gtt	2208						
321	Ser Ser Lys Pro Thr Asn Val Glu Ser Thr Ser Lys Ser His Asp Val							
322			725		730		735	
324	cat tca gca aat caa att gat tgc gag aaa gtg tgc gcg cag agc agc	2256						
325	His Ser Ala Asn Gln Ile Asp Cys Glu Lys Val Cys Ala Gln Ser Ser							
326			740		745		750	
328	gat aag cta aat aat cat ctg gcc gac aag att gtc gag aac aac aat	2304						
329	Asp Lys Leu Asn Asn His Leu Ala Asp Lys Ile Val Glu Asn Asn Asn							
330			755		760		765	
332	ttg gat ata ggc ggc cat gag gaa aag aag ttg gtt cat tcg ata agc	2352						
333	Leu Asp Ile Gly Gly His Glu Glu Lys Lys Leu Val His Ser Ile Ser							
334			770		775		780	
336	agc gaa gac tac aca caa atc aag gac aaa tcg aat gat ttc aca aaa	2400						
337	Ser Glu Asp Tyr Thr Gln Ile Lys Asp Lys Ser Asn Asp Phe Thr Lys							
338	785		790		795		800	
340	ttt aac gaa gcc ggc tac aaa att ctg caa att aaa agc gac agc tca	2448						
341	Phe Asn Glu Ala Gly Tyr Lys Ile Leu Gln Ile Lys Ser Asp Ser Ser							
342			805		810		815	
344	ctc atc tca tcg aag cta tac caa aag ggt ata cac aag gat aac ttg	2496						
345	Leu Ile Ser Ser Lys Leu Tyr Gln Lys Gly Ile His Lys Asp Asn Leu							
346			820		825		830	
348	gag cgt tcg cag aga ctt aca gag agt gtg aat acg att ccc gat aat	2544						
349	Glu Arg Ser Gln Arg Leu Thr Glu Ser Val Asn Thr Ile Pro Asp Asn							
350			835		840		845	
352	gcc acc gcc acc gcg gtg agc agc agc tca ctc acc aaa ttc aat ata	2592						
353	Ala Thr Ala Thr Ala Val Ser Ser Ser Ser Leu Thr Lys Phe Asn Ile							
354			850		855		860	
356	aat tca gca aag cca gcc gcc gcc gcc gat tcg cgt agc act gcc aca	2640						
357	Asn Ser Ala Lys Pro Ala Ala Ala Ala Asp Ser Arg Ser Thr Gly Thr							
358	865		870		875		880	
360	gat cca agt aca cca cag aac att cta cag att aaa gat ttg aat ttc	2688						
361	Asp Pro Ser Thr Pro Gln Asn Ile Leu Gln Ile Lys Asp Leu Asn Phe							
362			885		890		895	

VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date